

FIG. 1

mRNA Expression Profiles of A34

End point RT-PCR

Stomach Testis



Origene cDNA Panel (24 Normal Tissues)

FIG. 2
Analysis of A34 mRNA Expression in Normal and Malignant Tissues

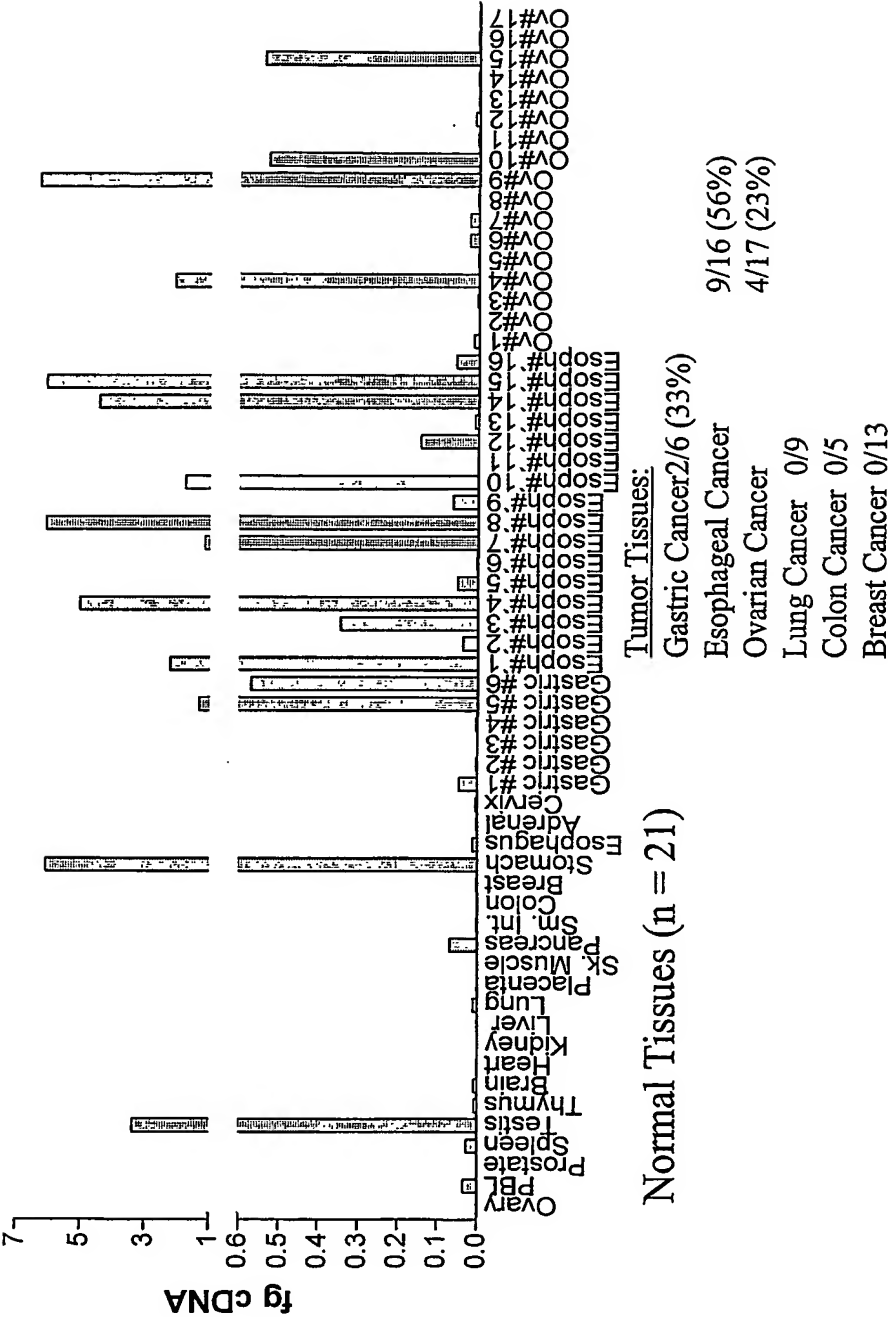


FIG. 3

A34 Protein: A34 vs A33

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1  MVFAFWKVFLILSLAGQSVVQVTIPDGFVNVTGNSVNTLICIYTTTIVASREQLSIQWS      A34
1  MVGKMWPVLWTLCAVRVTVDALSVETPDQDVLRSQCKSVTLPCITYHTSTSSREGL-IQWD      A33
   MV  W  V  L      V      V  P      G  VTL  C  Y  T      SRE  L  IQW
61  FFHKKEMEPISIFYSQGGQAVAIQGFKDRITGSN--DPGNASITISHMQPADSGIYICDV      A34
60  KLLLTHTERVVIWPFNSKNYIHGELYKNRVVISNNAEQSDASITIDQLTMADNGTYECSV      A33
   I      K  R  SN      ASITI      AD  G  Y  C  V
119  NNPPDFLGQNQGILNVSVLVKPSKPLCSVQGRPETGHTISLCLSLALGTPSPVYYWHKLE      A34
120  SLMSDLEGNTKSRVRLVLVPPSKPECGIEGETIIGNNIQLTCQSKESPTPQYSWKRY-      A33
   D  G      VLV  PSKP  C  G      G  I  L  C  S  G  P  P  Y  W
179  GRDIVPVKENF-NPTTGILV-IGNLTNFEQGYQCTAINRLGNSSCEIDLTSSHPEVGII      A34
179  --NILNQEQLAQPASGQPVSLKNISTDTSGYIYICTSSNEEGTQFCNITVAVRSPSMNVA      A33
   I      P  G  V  N      GYV  CT  N  G  C  I      P
237  --VGALIGSLVGAAIIISVVCFARNKAKAKAKERNKSKTIAELEPMTKINPRGESEAMPRE      A34
237  LYVGI AVG-VVAALIIIGIIYYCCC---CRGKD-----A33
   VG  G  V  A  III      K
295  DATQLEVTLPSSIHETGPDTTIQEPDYEPKTQEPAPEPAPGSEPMAVPDLIDIELELEPET      A34
266  -----DNTEDKE-DARNREAYEEP-----PEQLRELSREREE      A33
   D      P  E  EP      P      EL  E  E
355  QSELEPEPEPESEPGVVVEPLSEDEKGVVKA      A34
298  EDDYRQEEQORSTGRES---PDHLDQ-----A33
   E      L

```

A34: Nucleic acid sequence (SEQ ID NO: 3):

CTTCTTGTGGTAGGGACCTCTCCTCAGTATTTGAAACTAACCAGCATCTGACAGA
TTTCGAATTTGTAAAAAATACCCTCGAAGATTCAGGAATGAAGCTTCTGTGTGAA
GGATTAAAACAGCCCAACTGTGTATTACAGACATTGAGGTGGTACCGGTGCCTTA
TCTCTTCTGCTTCTTGTGGGGCTCTAGCAGCTGTTCTTAGCACCAGTCAGTGGCT
CACTGAACTGGAATTTAGTGAGACAAAACCTGGAAGCTTCAGCTTTGAAATTGCTC
TATGGAGGCTTAAAAGATCCAAATTGCAAATTACAGAAGCTCAACTTGCAGTTTTT
CTTTATCTGTAAACCGCTGCAAACTTCCAGTTGGAATGGTTGGAATTGTTCTGG
TTTCTCGGGATCATTGGTGCAATCTCATTTTGGCTACTGTTCAGGACAGTTCTTTC
AAATGTGATCTTTGTAAGCTGCTCTGGCCTTCCACCAGAGTTGCTGCTGCAAAGG
ATTGTGGGAGTCCTAAGTCCTTCCATATCAGAAGGGCTGAACTGGGCAGGAAGACT
TGAGGCAGTGGAGGAGGTTTTTGGGGTGTGGGGGTGCTTGTACAGCCCGGTGACCCA
GCATCTCAGGGTGGGGGGCATTGTGAAAACATATGGGTCTTTTAGAGACTTGGTGG
ACTTAGAAGTCAAGGCAGAACCAAGCCTGAGAAAAGGTGGTATGGATCTCCAGAG
ACCCACCTTACAAGTTGTCTCCTTTGCAAAATCTTCTCCCTCAAACATTTTCTC
TTTATTGCATTGCCTAATTCTCCTGGTCAGGTTAGTGTGGTGCAAGTGACCATCC
CAGACGGTTTTCTGTAACGTGACTGTTGGATCTAATGTCACTCTCATCTGCATCTA
CACCACCACTGTGGCCTCCCGAGAACAGCTTTCCATCCAGTGGTCTTTCTTCCAT
AAGAAGGAGATGGAGCCAATTTCTATTTACTTTTCTCAAGGTGGACAAGCTGTAG
CCATCGGGCAATTTAAAGATCGAATTACAGGGTCCAACGATCCAGGTAATGCATC
TATCACTATCTCGCATATGCAGCCAGCAGACAGTGGAAATTTACATCTGCGATGTT
AACAAACCCCCAGACTTTCTCGGCCAAAACCAAGGCATCCTCAACGTCAAGTGTGT
TAGTGAAACCTTCTAAGCCCCCTTGTAGCGTTCAAGGAAGACCAGAACTGGCCA
CACTATTTCCCTTTCTGTCTCTCTGCGCTTGGAACACCTTCCCCTGTGTACTAC
TGGCATAAACTTGAGGGAAGAGACATCGTGCCAGTGAAAGAAAACCTTCAACCCAA
CCACCGGGATTTTGGTCATTGGAAATCTGACAAATTTTGAACAAGGTTATTACCA
GTGTACTGCCATCAACAGACTTGGCAATAGTTCCTGCGAAATCGATCTCACTTCT
TCACATCCAGAAGTTGGAATCATTGTTGGGGCCTTGATTGGTAGCCTGGTAGGTG
CCGCCATCATCATCTCTGTTGTGTGCTTCGCAAGGAATAAGGCAAAAGCAAAGGC
AAAAGAAAGAAATTCTAAGACCATCGCGGAACCTTGAGCCAATGACAAAGATAAAC
CCAAGGGGAGAAAGCGAAGCAATGCCAAGAGAAGACGCTACCCAAGTAGAAGTAA
CTCTACCATCTTCCATTCATGAGACTGGCCCTGATACCATCCAAGAACCAGACTA
TGAGCCAAGGCCTACTCAGGAGCCTGCCCCAGAGCCTGCCCCAGGATCAGAGCCT
ATGGCAGTGCCTGACCTTGACATCGAGCTGGAGCTGGAGCCAGAAACGCAGTCGG
AATTGGAGCCAGAGCCAGAGCCAGAGCCAGAGTCAGAGCCTGGGGTTGTAGTTGA
GCCCTTAAGTGAAGATGAAAAGGGAGTGGTTAAGGCATAG

A34 amino acid sequence (SEQ ID NO: 4):

MDLQRPTLQVLLCKIFSLKFLFIALPNSPGQVSVVQVTIPDGFVNVTVGSNVT
LICIYTTTVASREQLSIQWSFFHKKEMEPISIIYFSQGGQAVAIGQFKDRITGSND
PGNASITISHMQPADSGIYICDVNNPPDFLGQNQGILNVSVLVKPSKPLCSVQGR
PETGHTISLSLSALGTPSPVYYWHKLEGRDIVPVKENFNPTTGILVIGNLTNFE
QGYQCTAINRLGNSSCEIDLTSSHPEVGIIVGALIGSLVGAIIISVVCFARNK
AKAKAKERNKTI AELEPMTKINPRGESEAMPREDATQLEVTLPPSSIHETGPDIT
QEPDYEKPTQEPAPEPAPGSEPMVDPDLIELELEPETQSELEPEPEPEPESEPE
GVVVEPLSEDEKGVVKA

FIG. 4

A34 clone nucleic acid sequence (SEQ. ID NO: 5)

ACTGTTGGATCTAATGTCACTCTCATCTGCATCTACACCACCACTGTGGCCTCCCGAGA
ACAGCTTTTCCATCCAGTGGTCTTTCTTCCATAAGAAGGAGATGGAGCCAATTTCTATTT
ACTTTTCTCAAGGTGGACAAGCTGTAGCCATCGGGCAATTTAAAGATCGAATTACAGGG
TCCAACGATCCAGGTAATGCATCTATCACTATCTCGCATATGCAGCCAGCAGACAGTGG
AATTTACATCTGCGATGTTAACAACCCCCCAGACTTTCTCGGCCAAAACCAAGGCATCC
TCAACGTCAGTGTGTTAGTGAAACCTTCTAAGCCCCCTTTGTAGCGTTCAAGGAAGACCA
GAAACTGGCCACACTATTTCCCTTTTCTGTCTCTCTGCGCTTGGAACACCTTCCCCTGT
GTACTACTGGCATAAACTTGAGGGAAGAGACATCGTGCCAGTGAAAGAAAACCTTCAACC
CAACCACCGGGATTTTGGTCATTGGAAATCTGACAAATTTTGAACAAGGTTATTACCAG
TGTA CTGCCATCAACAGACTTGGCAATAGTTCCTGCGAAATCGATCTCACTTCTTCACA
TCCAGAAGTTGGAATCATTGTTGGGGCCTTGATTGGTAGCCTGGTAGGTGCCGCCATCA
TCATCTCTGTTGTGTGCTTCGCAAGGAATAAGGCAAAAGCAAAGGCAAAAGAAAGAAAT
TCTAAGACCATCGCGGAACCTTGAGCCAATGACAAAGATAAACCCCAAGGGGAGAAAGCGA
AGCAATGCCAAGAGAAGACGCTACCCAACCTAGAAGTAACCTTACCATCTTCCATTCATG
AGACTGGCCCTGATACCATCCAAGAACCAGACTATGAGCCAAAGCCTACTCAGGAGCCT
GCCCCAGAGCCTGCCCCAGGATCAGAGCCTATGGCAGTGCCTGACCTTGACATCGAGCT
GGAGCTGGAGCCAGAAACGCAGTCGGAATTGGAGCCAGAGCCAGAGCCAGAGCCAGAGT
CAGAGCCTGGGGTTGTAGTTGAGCCCTTAAGTGAAGATGAAA

A34 clone amino acid sequence (SEQ. ID NO: 6)

TVGSNVTLCIYTTTVASREQLSIQWSFFHKKEMEPISIIYFSQGGQAVAIGQFKDRITG
SNDPGNASITISHMQPADSGIYICDVNNPPDFLGQNQGILNVSVLVKPSKPLCSVQGRP
ETGHTISLSCLSALGTPSPVYYWHKLEGRDIVPVKENFNPTTGILVIGNLTNFEQGYIQ
CTAINRLGNSSCEIDLTSSHPEVGIIVGALIGSLVGAAIIISVVCFARNKAKAKAKERN
SKTIAELEPMTKINPRGESEAMPREDATQLEVTLPPSIHETGPDTIQEPDYEKPTQEP
APEPAPGSEPMVDPDLIDIELELEPETQSELEPEPEPEPESEPGVVVEPLSEDE

FIGURE 5

A33-like 3 polynucleotide sequence (SEQ ID NO: 7):

TGTGCAGGCAACAGGAAACAAATACAGAGGGCAGAGCAAGGATTGGTCAGGACGG
GCTTAGTGAGAAAGGCTCTGAACGAGACACACACCAGCTGCAGCTTCGTACTGAC
GCCTGCCAGCTCCTACACACCTTCCTGGGCAACTGCCAGCGGGGCAAGGCAGGCC
TGGGGCCACCCTGCAGGCAGTGTCTGGGCCCTCAGCTCCCCCTCCCTCCACCTAC
CCCCTCACACCCACCCTACGACCCACGGGATACCCAGCCCAGACGGAGGAAAC
ACCGAGCCTAGAGACATGAGAGTTGGAGGAGCATTCACCTTCTACTCGTGTGCC
TGAGCCCAGCACTGCTGTCTGCTGTGCGGATCAACGGGGATGGACAGGAGGTCCT
GTACCTGGCAGAAGGTGATAATGTGAGGCTGGGCTGCCCCCTACGTCTGGACCCT
GAGGACTATGGTCCCAATGGGCTGGACATCGAGTGGATGCAGGTCAACTCAGACC
CCGCCCCACCAGAGAGAACGTGTTCTTAGTTACCAGGACAAGAGGATCAACCA
TGGCAGCCTTCCCCATCTGCAGCAGAGGGTCCGCTTTGCAGCCTCAGACCCAAGC
CAGTACGATGCCTCCATCAACCTCATGAACCTGCAGGTATCTGATACAGCCACTT
ATGAGTGCCGGGTGAAGAAGACCACCATGGCCACCCGGAAGGTCATTGTCACTGT
CCAAGCACGACCTGCAGTGCCCATGTGCTGGACAGAGGGCCACATGACATATGGC
AACGATGTGGTGCTGAAGTGCTATGCCAGTGGGGGCTCCCAGCCCCCTCTCCTACA
AGTGGGCCAAGATCAGTGGGCACCATACCCCTATCGAGCTGGGTCTTACACCTC
CCAGCACAGCTACCACTCAGAGCTGTCCTACCAGGAGTCCTTCCACAGCTCCATA
AACCAAGGCCTGAACAATGGGGACCTGGTGTGTAAGGATATCTCCAGAGCAGATG
ATGGGCTGTATCAGTGACAGTGGCCAACAACGTGGGCTACAGTGTGTTGTGTGGT
GGAGGTGAAGGTCTCAGACTCCCGCGGTATAGGCGTGATCATCGGCATCGTCTTG
GGCTCTCTGCTCGCGCTGGGCTGCCTGGCCAGAGGACGCCGTGGCGCCCGGGTGC
AAGGCCAGCGGGCGCGGCAGCCGCGTCACCCACCTCCTGGGGTACCCGACGCAGA
ACGTCAGCCGCTCCCTGCGCCGCAATACGCGCCTCCCCCTGCGGCGGCCCCGAG
GACGTGGCCCTGGCGCCCTGCACCGCCGCGCCGCTGCGAAGCGGGCCCCCTCC
CGGTCTACGTCAAGGTCAAGAGCGCGGAGCCGGCTGACTGCGCCGAGGGGCCGGT
GCAGTGCAAGAACGGCCTCTTGGTGTGA

A33-like 3 polypeptide sequence (SEQ ID NO: 8):

MRVGGAFHLLLVCLSPALLSAVRINGDGQEVLYLAEGDNVRLGCPYVLDPEDYGP
NGLDIEWMQVNSDPAHHRENVFLSYQDKRINHGSPLHLQQRVRFAASDPSQYDAS
INLMNLQVSDTATYECRVKKTMATRKVIITVQARPAVPMCWTEGHMTYGNDVVL
KCYASGGSQPLSYKWAKISGHHYPYRAGSYTSQHSYHSELSYQESFHSSINQGLN
NGDLVLKDISRADDGLYQCTVANNVGYSVCVVEVKVSDSRRIIGVIGIVLGSLLA
LGCLARGRRGARVQGQRARQPRHPPPGVPDAERQPLPAPQYAPPPCGGPEDVALA
PCTAAACEAGPSPVYVKVSAEPADCAEGPVQCKNGLLV

FIG. 6

A33-like 3 vs A33:

Score = 67.4 bits (163), Expect = 2e-10

Identities = 63/232 (27%), Positives = 95/232 (40%), Gaps = 35/232 (15%)

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Query: 29  QEVLYLAEGDNVRLGCPYVLDPEDYGPNGLDIEWMQVNSDPAHHRENVFLSYQDKRINHG 88
          Q+VL ++G +V L C Y          GL I+W ++      H   V   + +K   HG
A33  : 28  QDVLRASQGKSVTLPCYHTSTSSR--EGL-IQWDKLLL--THTERVVIWPFNSKNYIHG 82

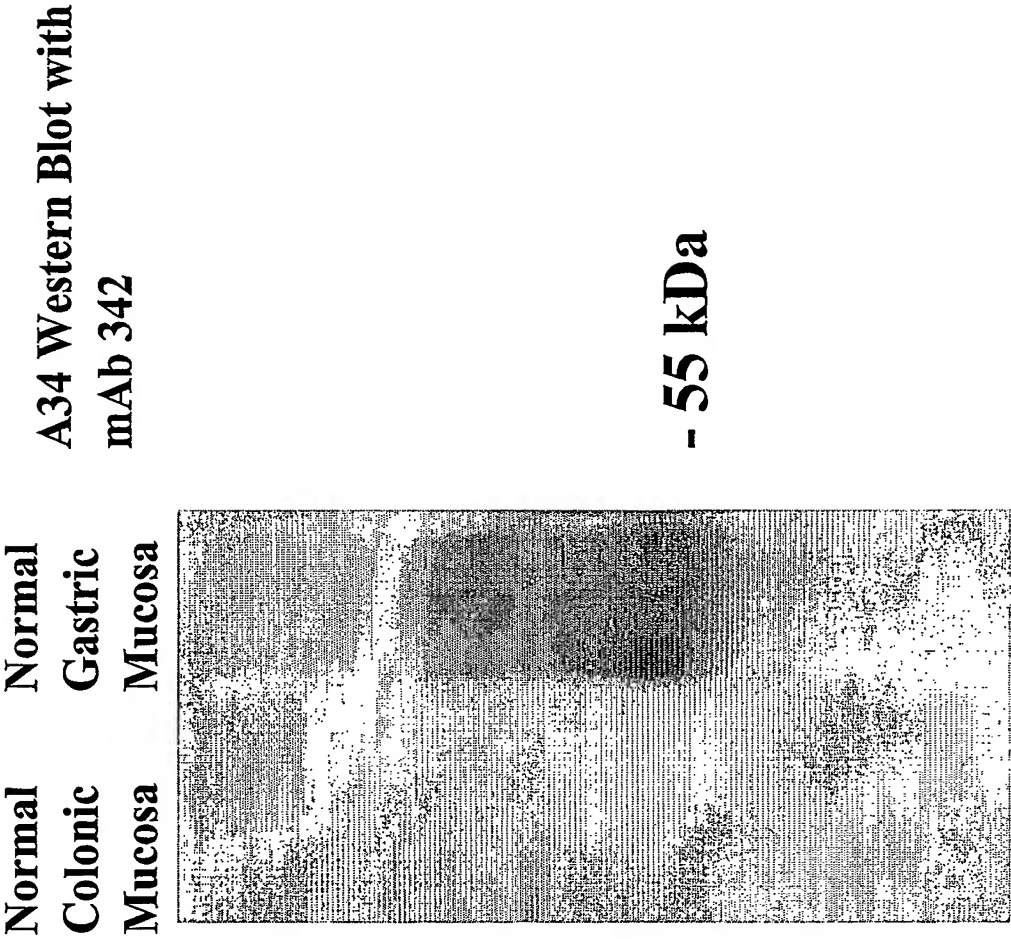
Query: 89  SLPHLQQRVRFAASDPSQYDASINLMNLQVSDTATYECRVKKT-----MATRKVIIVTVQA 144
          L   + RV + ++ Q DASI + L ++D TYEC V   +           +V + V
A33  : 83  EL--YKNRVSIS-NNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLVLV 139

Query: 145 RPAVPMCWTEGHMTYGNDDVVLKCYASGGSQPLSYKWAKISGHHYPYRAGSYTSQHSYHSE 204
          P+ P C EG   GN++ L C + GS   Y W + +
A33  : 140 PPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYN----- 179

Query: 205 LSYQESFHSSINQGLNNGDLVLKDISRADDGLYQCTVANNVGYSVCVVEVKV 256 (SEQ. ID NO: 9)
          + QE   + Q +   + LK+IS   G Y CT +N G   C + V V
A33  : 180 ILNQE--QPLAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAV 228 (SEQ. ID NO: 10)
```

FIG. 7

FIG. 8



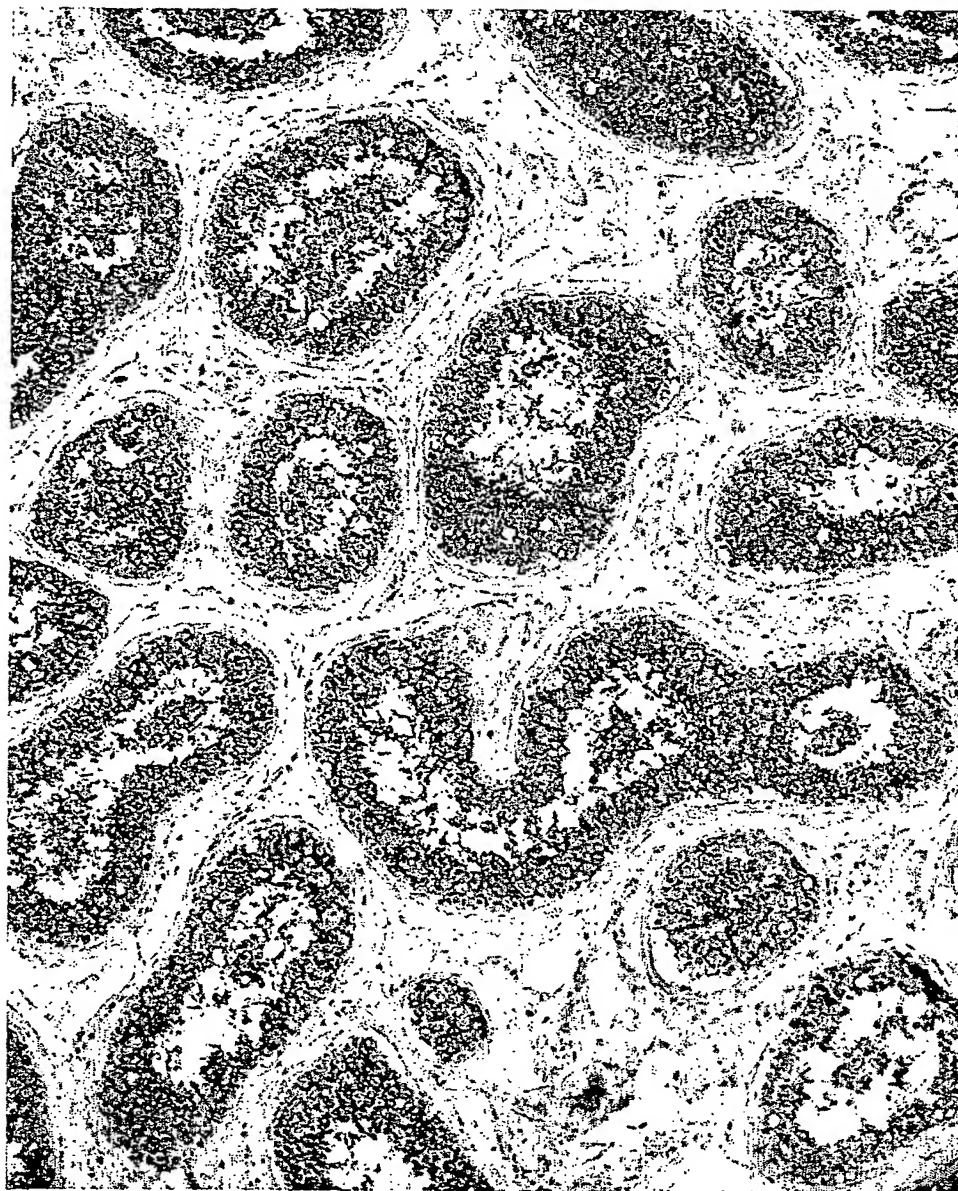


FIG. 9

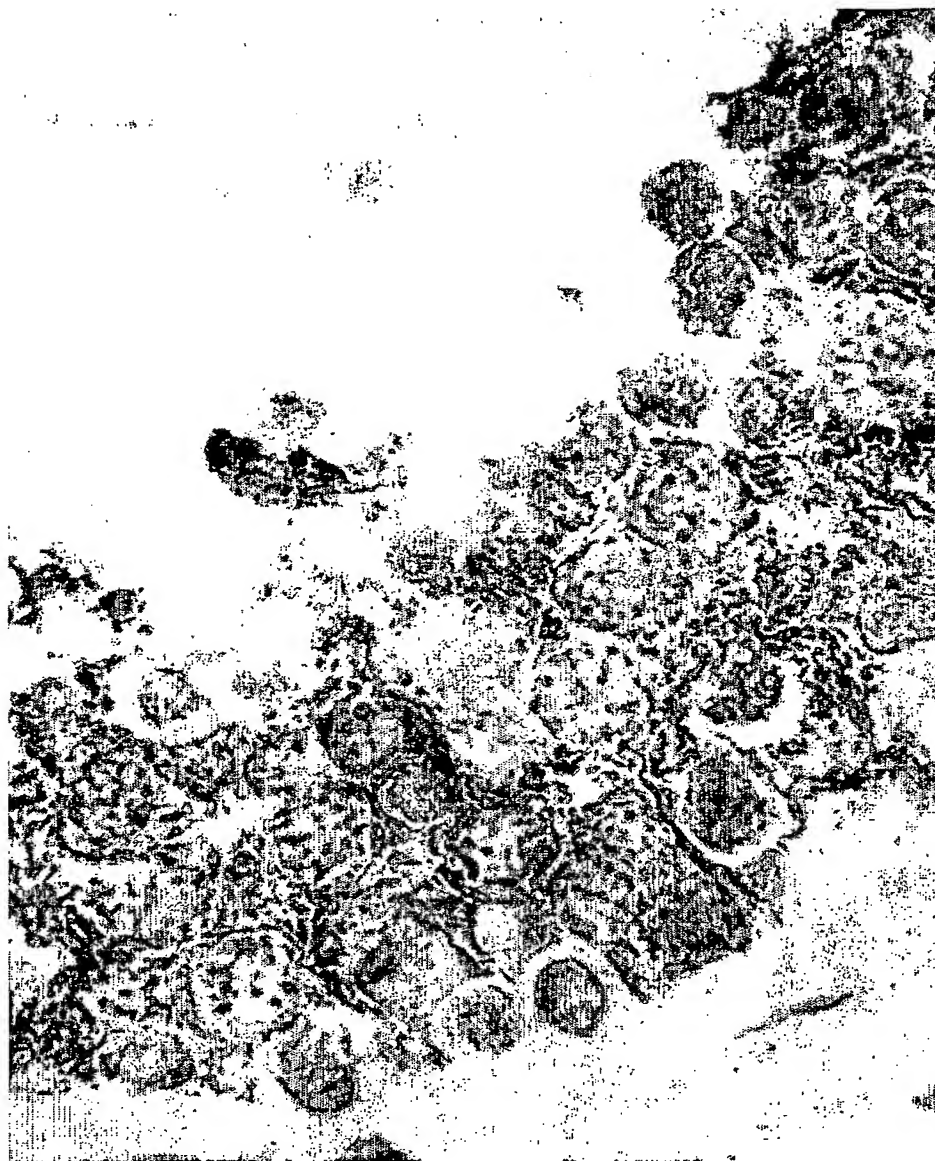


FIG. 10

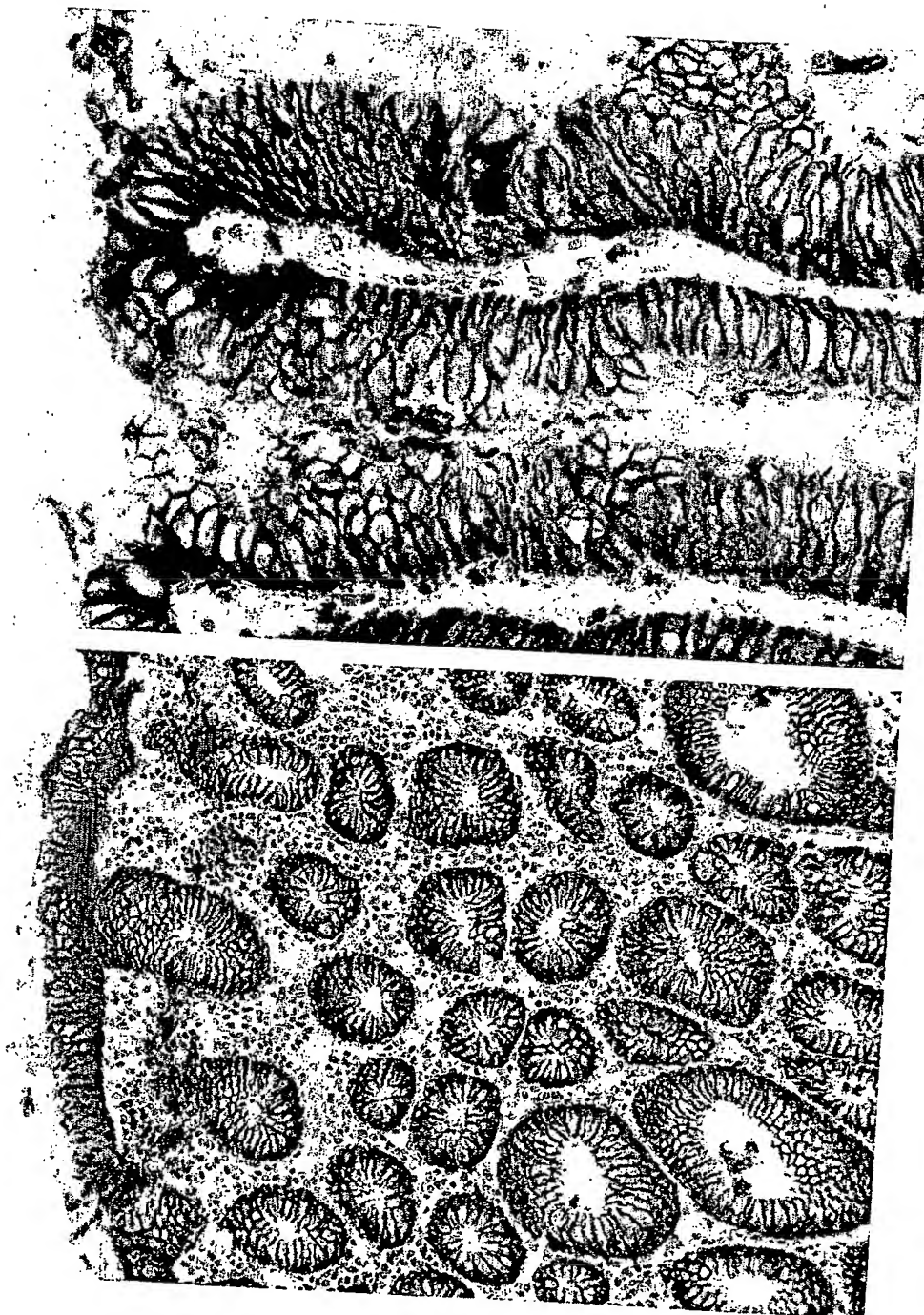


FIG. 11



FIG. 12



FIG. 14



FIG. 13

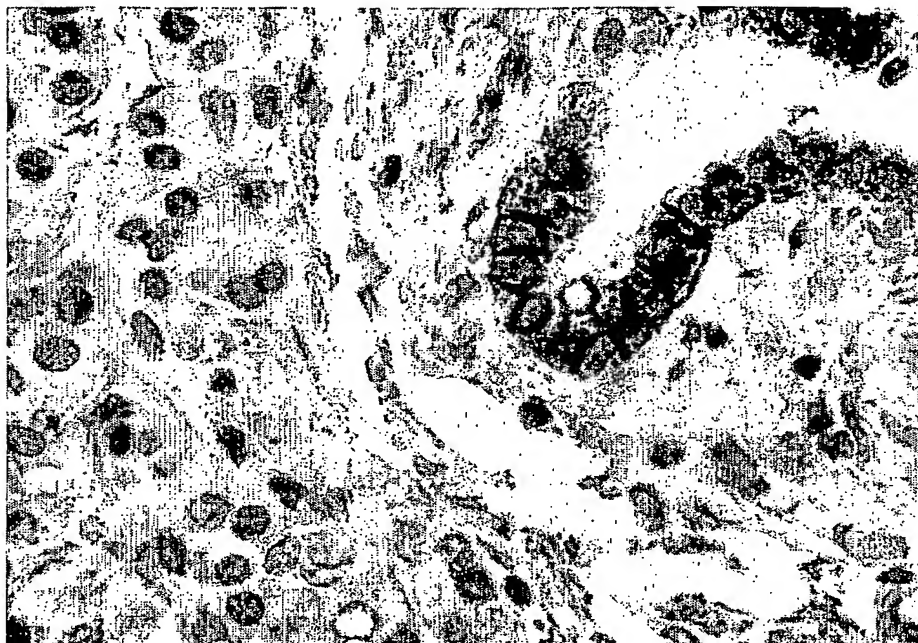


FIG. 16

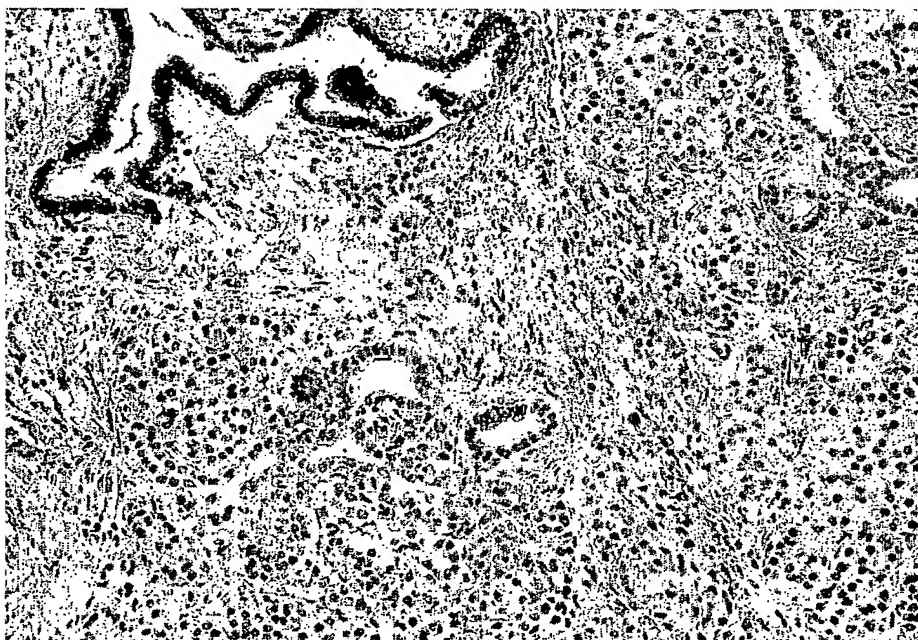


FIG. 15

FIG. 17

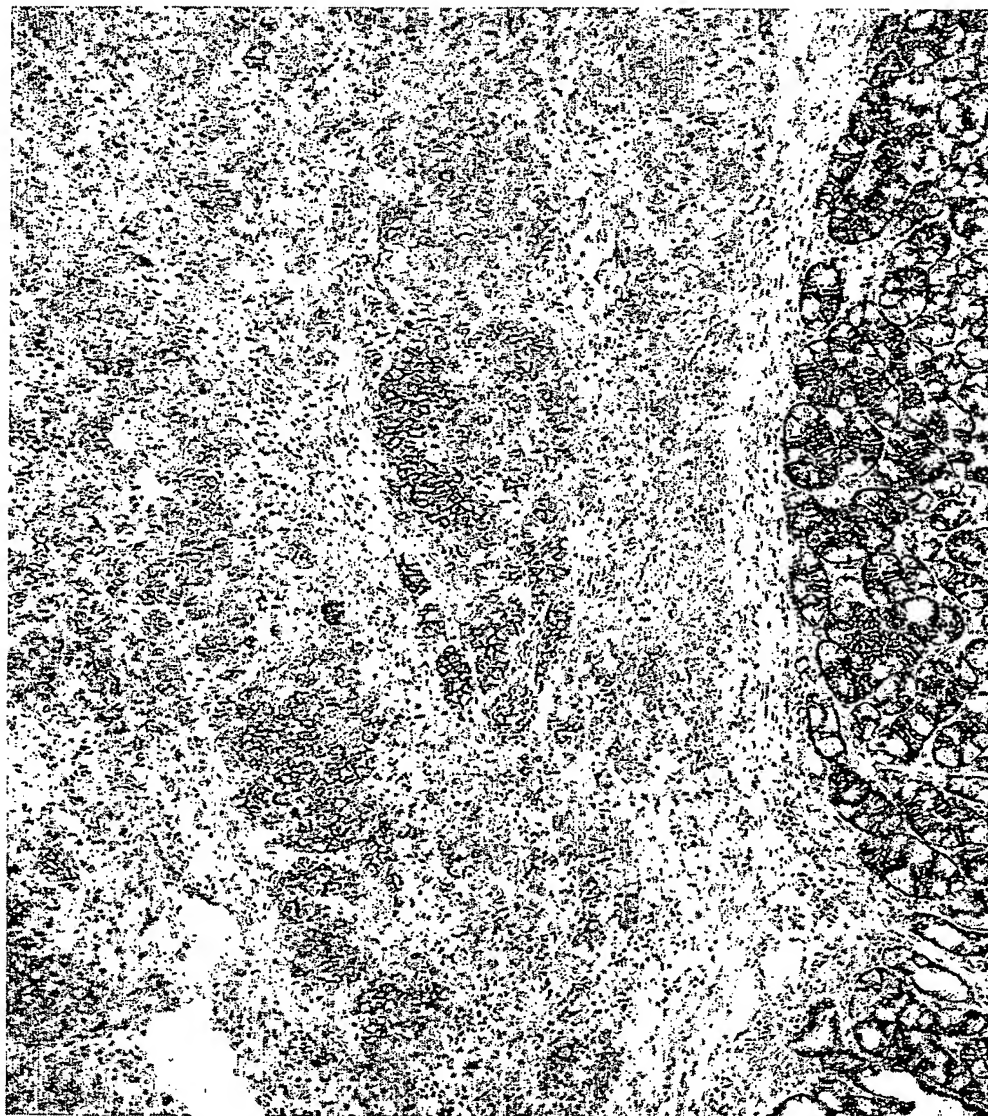


FIG. 18

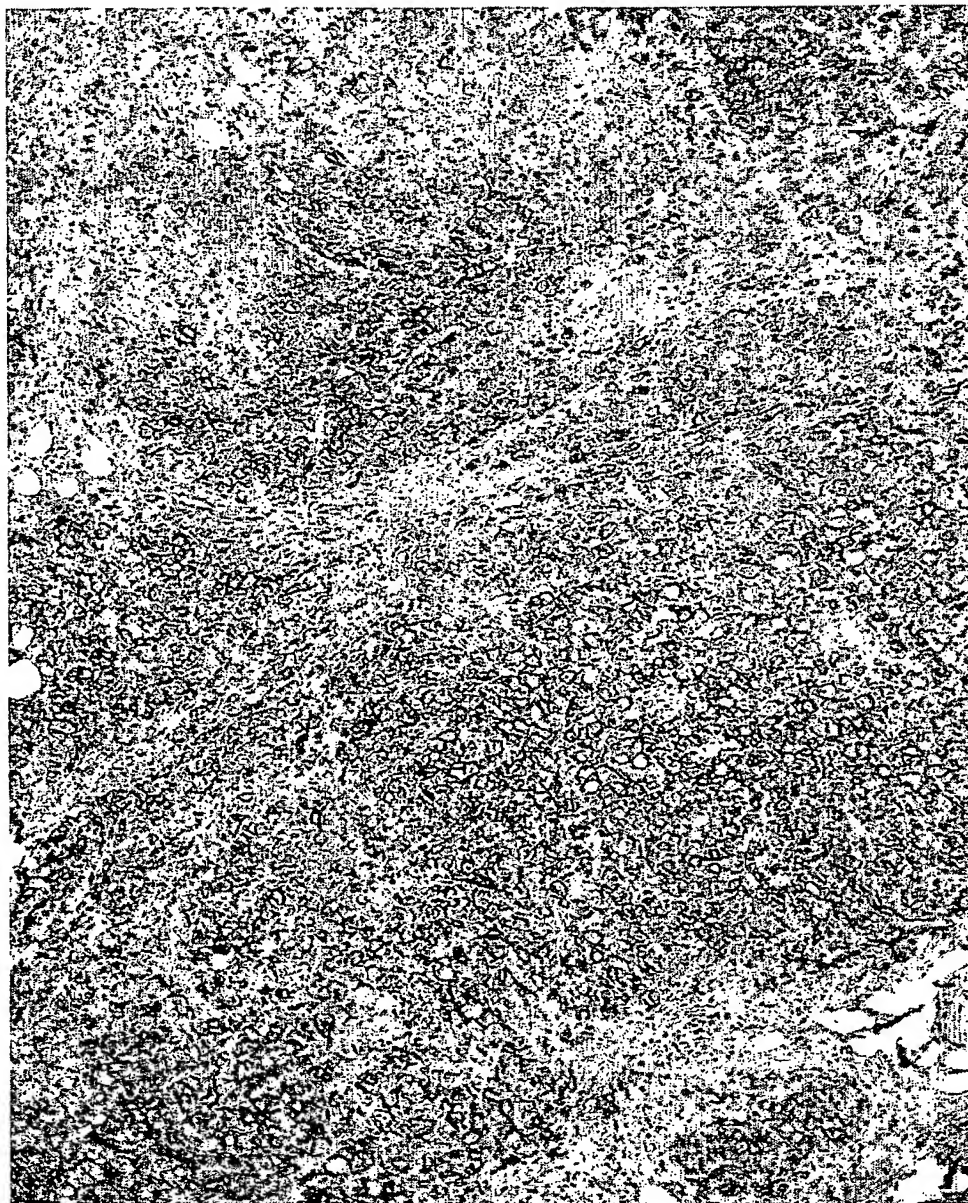
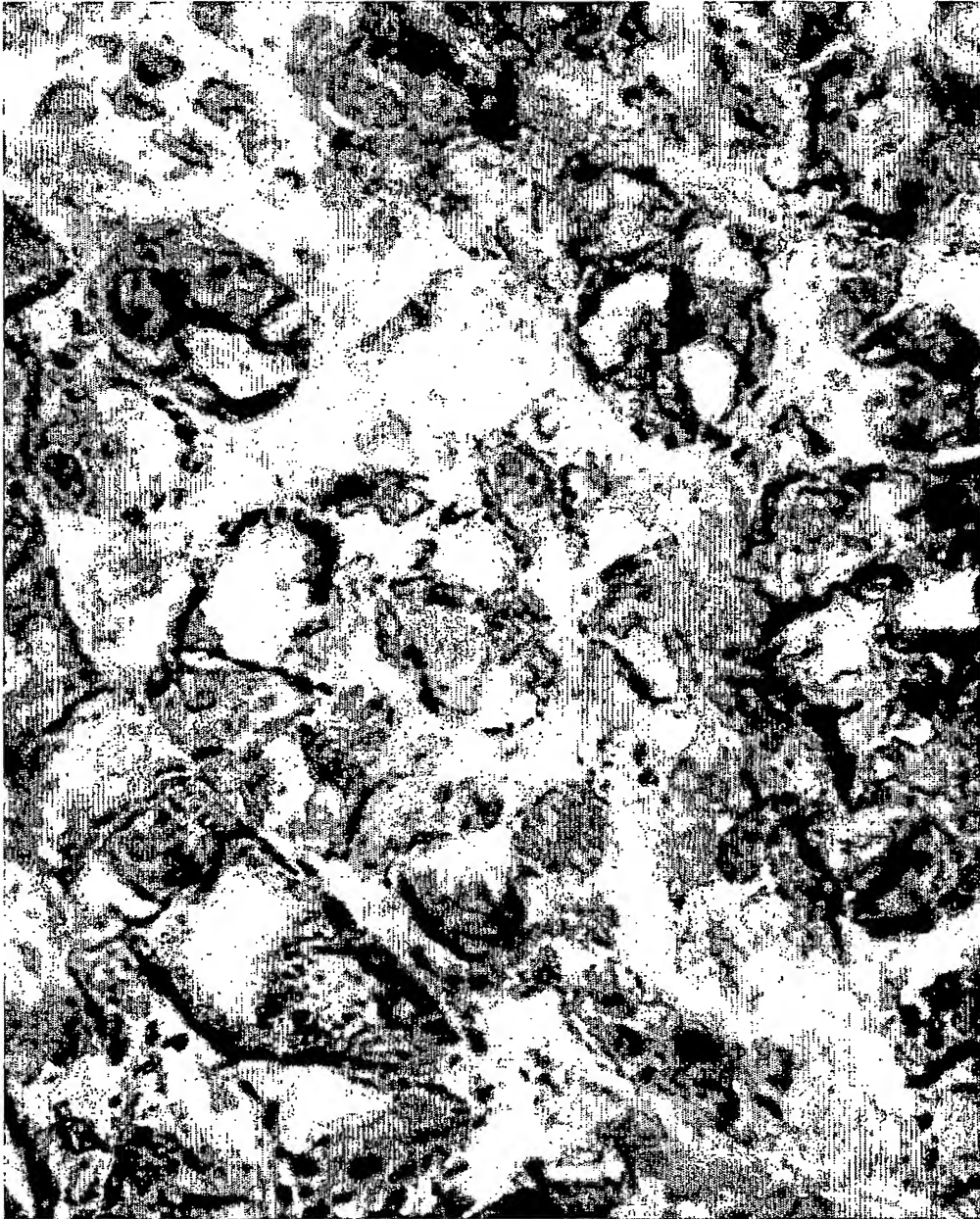


FIG. 19



FIG. 20



TA-BI-mur.A34 Light Chain Clone: 209-970

atgaggtgccttggttcagtttctggggctgcttgctctggatccct
M R C L V Q F L G L L V L W F P
ggagccattggggatattgtgatgactcaggctgcaccctctgtccctgtcactcctgga
G A I G D I V M T Q A A P S V P V T P G
gagtcagtatccatctcctgcaggctctagtagcagtcctcctgcatactgaatggcaacact
E S V S I S C R S S T S L L H S N G N T
tacttctattgggttcctgcagaggccaggccagtcctcctcagtcctgatatatcggtatg
Y L Y W F L Q R P G Q S P Q L L I Y R M
tccaaccttgcctcaggagtcaccagacaggttcagtgggcagtgggtcaggaactgctttc
S N L A S G V P D R F S G S G S G T A F
acactgagaatcagtagagtgaggctgaggatgtgggtatttattactgt
T L R I S R V E A E D V G I Y Y C M Q H
ttcggaggggggaccaaactggaaataaaacgg
L E Y P F T F G G G T K L E I K R

(SEQ ID NO: 20)

(SEQ ID NO: 21)

TA-BI-A34 Heavy Chain 4 Clone: 209-970

atgaactttgggttcagcttggttttccttgccttatttttaaagggt
M N F G F S L V F L A L I L K G
gtccagtgtagggtggagctggtggagctctgggggaggcctagtgacgcctggaggggtcc
V Q C E V E L V E S G G G L V Q P G G S
ctgaaactctcctgtgcagcctctggattcaccttcagtaactttggcatgcttgggtt
L K L S C A A S G F T F S T F G M S W V
cgccagactccagacaagaggctggagttggtcgcaaccattaatagtaatggtgtagg
R Q T P D K R L E L V A T I N S N G G R
acctattatctagacagtggtgaaggggcgattcaccatctccagagaaaatgccagaac
T Y Y L D S V K G R F T I S R E N A K N
accctgtacctgcaaagtgcagcagtcgaagtctgaggacacagccatgtattactgtgca
T L Y L Q M S S L K S E D T A M Y Y C A
agaactgggggccaagggactctg
R D G G L L R D S A W F A Y W G Q G T L
gtcactgtctctgca (SEQ ID NO: 22)
V T V S A (SEQ ID NO: 23)

FIG. 21

TA-B1-mur.A34 Light Chain Clone: 209-564

atgaggtgccttgctcagcttctggggctgcttgctctggatccct
M R C L A Q L L C L L V L W I P
ggagccattggggatattgtgatgactcaggctgcaccctctgtacctgtcactcctgga
G A I G D I V M T Q A A P S V P V T P G
gagtcagtatccatctcctgcaggtctagtagcaggtctcctgcatggtaatggcaact
E S V S I S C R S S T S L L H G N G N T
tactgtatgggttcctgcagaggccaggccaggtctcctcagctcctgatatatcgga
Y L Y W F L Q R P G Q S P Q L L I Y R M
tccaaccttgctcagggagtcaccagacaggttcagtggcagtgggtcaggaactgctt
S N L A S G V P D R F S G S G S G T A F
acactgagaatcagtagagtggaggctgaggatgtgggtatttattactgt
T L R I S R V E A E D V G I Y Y C M Q H
ttcggaggggggaccaagctggaaataaaacgg
L E Y P F T F G G G T K L E I K R
(SEQ ID NO: 24)
(SEQ ID NO: 25)

TA-B1-A34 Heavy Chain 4 Clone: 209-564

atggactttgggttcagcttggttttccttgcccttatttttaaaggt
M D F G F S L V F L A L I L K G
gtccagtgtgaggtggagctggtggagtctgggggaggcttagtgcagcctggagggtcc
V Q C E V E L V E S G G G L V Q P G G S
ctgaaactctcctgtgcagcctctggattcaccttcagtaacatggcatgcttgggt
L K L S C A A S G F T F S S Y G M S W V
cgccagactccagacaagaggctggagttggtcgcaaccattaatagtaatgggtggtagg
R Q T P D K R L E L V A T I N S N G G R
acctattatctagacagtggaagggccgattcaccatctccagagacaatgccaagaac
T Y Y L D S V K G R F T I S R D N A K N
accctgtacctgcaaatgagcagctctgaagtctgaggacacagccatgtattactgtgca
T L Y L Q M S S L K S E D T A M Y Y C A
aga tggggccaagggactctg
R D G G L L R D S A W F A Y W G Q G T L
gtcactgtctctgca
V T V S A
(SEQ ID NO: 26)
(SEQ ID NO: 27)

FIG. 22

TA-B1-mur.A34 Light Chain Clone: 209-342

[illegible]

TA-B1-mur.A34 Heavy Chain Clone:209-342

atgggatggagctatatatcatctcttcttctggttagcaacagctacaggt
M G W S Y I I F F L V A T A T G
gtgcactcccaggtccagctgcagcagctctgggcctgagctgggtgaggcctgggggtctca
V H S Q V Q L Q Q S G P E L V R P G V S
gtgaagatttcctgcaagggttccggctacacattcactgatgatgctaacgcaactggggtg
V K I S C K G S G Y T F T D Y A T H W V
aggcagagtcattgcaaagagtcctagagtggtattggagttattagtagttactctggtaat
R Q S H A K S L E W I G V I S S Y S G N
acaaagtacaaccagaactttaaaggacaaggccacaatgactgtagacaaatcctccagc
T K Y N Q N F K D K A T M T V D K S S S
acagcctatatggaacttgccagattgacatctgaggattctgccatgtattactgtgca
T A Y M E L A R L T S E D S A M Y Y C A
agaatgggggtcaaggaacctcagtc
R Y D Y D V R Y Y A M D Y W G Q G T S V
accgtctcctca (SEQ ID NO: 30)
T V S S (SEQ ID NO: 31)

FIG. 23

TA-BI-mur.A34 light chain clone 209-970

CDR1: SNGNTYLY	(SEQ ID NO: 32)
CDR2: RMSNLAS	(SEQ ID NO: 33)
CDR3: MQHLEYPFT	(SEQ ID NO: 34)

TA-BI-A34 heavy chain clone 4 209-970

CDR1: TFGMS	(SEQ ID NO: 35)
CDR2: TINSNGGRTYYLDSVKG	(SEQ ID NO: 36)
CDR3: DGGLLRDSAWFAY	(SEQ ID NO: 37)

TA-BI-mur.A34 light chain clone 209-564

CDR1: GNGNTYLY	(SEQ ID NO: 38)
CDR2: RMSNLAS	(SEQ ID NO: 39)
CDR3: MQHLEYPFT	(SEQ ID NO: 40)

TA-BI-A34 heavy chain clone 4 209-564

CDR1: SYGMS	(SEQ ID NO: 41)
CDR2: TINSNGGRTYYLDSVKG	(SEQ ID NO: 42)
CDR3: DGGLLRDSAWFAY	(SEQ ID NO: 43)

TA-BI-mur.A34 light chain clone 209-342

CDR1: QATQDIVKNLN	(SEQ ID NO: 44)
CDR2: YATELAE	(SEQ ID NO: 45)
CDR3: LQFYDFPLT	(SEQ ID NO: 46)

TA-BI-mur.A34 heavy chain clone 209-342

CDR1: DYATH	(SEQ ID NO: 47)
CDR2: VISSYSGNT	(SEQ ID NO: 48)
CDR3: YDYDVRYAMDY	(SEQ ID NO: 49)

FIG. 24

AGCGGGGCGATGCCAGCAGATAAGCCAGGCAAACCTCGGTGTGATCGAAGAAGCCAATTTG
AGACTCAGCCTAGTCCAGGCAAGCTACTGGCACCTGCTGCTCTCAACTAACCTCCACACAAT
GGTGTTCGCATTTTGGGAAGGTCTTCTGATCCTAAGCTGCCTTGCAGGTCAGGTTAGTGTGG
TGCAAGTGACCATCCCAGACGGTTTCGTGAACGTGACTGTTGGATCTAATGTCACTCTCATC
TGCATCTACACCACCACTGTGGCCTCCCGAGAACAGCTTTCATCCAGTGGTCTTTCTTCCA
TAAGAAGGAGATGGAGCCAATTTCTATTTACTTTTCTCAAGGTGGACAAGCTGTAGCCATCG
GGCAATTTAAAGATCGAATTACAGGGTCCAACGATCCAGGTAATGCATCTATCACTATCTCG
CATATGCAGCCAGCAGACAGTGGAATTTACATCTGCGATGTTAACAACCCCCCAGACTTTCT
CGGCCAAAACCAAGGCATCCTCAACGTCAAGTGTGTAGTGAAACCTTCTAAGCCCCCTTGTA
GCGTTCAAGGAAGACCAGAACTGGCCACACTATTTCCCTTCTGTCTCTCTGCGCTTGGA
ACACCTTCCCCTGTGTACTACTGGCATAAACTTGAGGGAAGAGACATCGTGCCAGTGAAAGA
AACTTCAACCCAACCACCGGGATTTTGGTCATTGGAAATCTGACAAATTTTGAACAAGGT
ATTACCAGTGTACTGCCATCAACAGACTTGGCAATAGTTCCTGCGAAATCGATCTCACTTCT
TCACATCCAGAAGTTGGAATCATTGTTGGGGCCTTGATTGGTAGCCTGGTAGGTGCCGCCAT
CATCATCTCTGTTGTGTGCTTCGCAAGGAATAAGGCAAAAGCAAAGGCAAAAGAAAGAAAT
CTAAGACCATCGCGGAACCTTGAGCCAATGACAAAGATAAACCCAAGGGGAGAAAGCGAAGCA
ATGCCAAGAGAAGACGCTACCCAAGTAGAAGTAAGTCTACCATCTTCCATTTCATGAGACTGG
CCCTGATACCATCCAAGAACCAGACTATGAGCCAAAGCCTACTCAGGAGCCTGCCCCAGAGC
CTGCCCCAGGATCAGAGCCTATGGCAGTGCCTGACCTTGACATCGAGCTGGAGCTGGAGCCA
GAAACGCAGTCGGAATTGGAGCCAGAGCCAGAGCCAGAGCCAGAGTCAGAGCCTGGGGTTGT
AGTTGAGCCCTTAAGTGAAGATGAAAAGGGAGTGGTTAAGGCATAGGCTGGTGGCCTAAGTA
CAGCATTAATCATTAAAGGAACCCATTACTGCCATTTGGAATTCAAATAACCTAACCAACCTC
CACCTCCTCCTTCCATTTTGACCAACCTTCTTCTAACAAGGTGCTCATTCTACTATGAATC
CAGAATAAACACGCCAAGATAACAGCTAAATCAGCAAGGGTTCCTGTATTACCAATATAGAA
TACTAACAATTTTACTAACACGTAAGCATAACAAATGACAGGGCAAGTGATTTCTAACTTAG
TTGAGTTTTTGCAACAGTACCTGTGTTGTTATTTTCAGAAAATATTATTTCTCTCTTTTAACT
ACTCTTTTTTTTTTATTTTGGACAGAGTCTTGCTCCGTCGCGCAGGCTGTGATCGTAGTGGTG
CGATCTCGGCTCACTGCGGCCTCCGCTCCCTGGGTTTCGGGCGATTCTCCTGCCTGGGCCTCC
TGAGTGGCTGGGACTGCAGGCACGTGCCGCCACGCCCGGCTAATTTTTTTGTATTTTGGTAG
AGATGGGGTTTCACGTTGTTGGCCAGGATGGTCTCCATCTCCTGACCTCATGATCCGCCCAC
CTTGGCCTCCCAAATGCTGGGATTACAGGCATGAGCCACTGCGCCCGGCCTCTTTTAGCT
ACTCTTATGTTCCACATGCACATATGACAAGGTGGCATTAATTAGATTCAATATTATTTCTA
GGAATAGTTCCTCATTCATTTTTTATATTGACCCTAAGAAAATAATTTCATCAGCATTATCTC
ATAGATTGGAATAATTTTCTCCAAATACAATAGAGGAGAATATGTAAAGGGTATACATTAATT
GGTACGTAGCATTTAAAATCAGGTCTTATAATTAATGCTTCATTCTCATATTAGATTTCCC
AAGAAATCACCTTGGTATCCAATATCTGAGCATGGCAAATTTAAAAAATAACACAATTTCTT
GCCTGTGACCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGGGTTCTGA
GACCAGCCTGGCCGACATGGCGAAGCCCCTTCTCTGCTAGGAATGCAGAAATTGGCTGGGCG
TGGTGGTGCATGCCGTGTAGTCCCGGCTACTTGGGAGGCTGAGGCAGGAGAGTCGCTTGAACC
CAGGGGGTGGAGGTTGCAGTGAGCCGAGATTGTGCCACTGCACTCCAACCTGGGTGACGGAG
TGAGATTCCATCTGAAAAACAAAAACAAAAACAGAAAAACAAACAAACAAAAACAAAAATC
CCCACAACCTTTGTCAAATAATGTACAGGCAACACTTTCAAATATAATTTCTTTCAGTGAAT
ACAAAATGTTGATATCATAGGTGATGTACAATTTAGTTTTGAATGAGTTATTATGTTATCAC
TGTGTCTGATGTTATCTACTTTGAAAGGCAGTCCAGAAAAGTGTCTAAGTGAAGTCTTAAG
ATCTATTTTAGATAATTTCAACTAATTAATAACCTGTTTTACTGCCTGTACATTCCACATT
AATAAAGCGATACCAATCTTATATGAATGCTAATATTACTAAAATGCACTGATATCACTTCT
TCTTCCACTGTTGAAAAGCTTTCTCATGATCATATTTACCCACATCTCACCTTGAAGAAAC
TTACAGGTAGACTTACCTTTTCACTTGTGGAATTAATCATATTTAAATCTTACTTTAAGGCT
CAATAAATAATACTCATAATGTCCCAAAAAAAAAAAAAAAAAA (A34, SEQ ID
NO: 50)

FIG. 25

MVFAPWKVFLILSCLAGQVSVVQVTIPDGFVNVTVGSNVTLICITYTTTVAEREQLSIQWSFF
HKKEMEPISIIYFSQGGQAVAIGQFKDRITGSNDPGNASITISHMQPADSGIYICDVNNPPDF
LGQNQGILNVSVLVKPSKPLCSVQGRPETGHTISLSCLALGTPSPVYYWHKLEGRDIVPVK
ENFNPTTGILVIGNLTNFEQGYQCTAINRLGNSSCEIDLTSSHPEVGIIVGALIGSLVGAA
IIISVVCFARNKAKAKAKERNKSTIAELEPMTKINPRGESEAMPREDATQLEVTLPSSIHET
GPDTIQEPDYEPKPTQEPAPAPGSEPMAVPDLDIELELEPETQSELEPEPEPEPESEPGV
VVEPLSEDEKGVVKA (A34, SEQ ID NO: 1)

FIG. 26